

SequenceListing-73670826.txt  
SEQUENCE LISTING

<110> BEBBINGTON, CHRISTOPHER ROBERT  
YU, BO

<120> TRANSACTIVATION SYSTEM FOR MAMMALIAN CELLS

<130> 73678-026

<140> 10/585,149  
<141> 2006-06-30

<150> PCT/US2004/043830  
<151> 2004-12-30

<150> 60/533,917  
<151> 2003-12-13

<160> 56

<170> PatentIn version 3.5

<210> 1  
<211> 236  
<212> PRT  
<213> Cricetulus longicaudatus

<400> 1  
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1 5 10 15

Lys Tyr Ile His Tyr Lys Leu Ser Gln Arg Gly Tyr Glu Trp Asp Val  
20 25 30

Gly Asp Val Asp Ala Ala Pro Leu Gly Ala Ala Pro Thr Pro Gly Ile  
35 40 45

Phe Ser Phe Gln Pro Glu Ser Asn Pro Thr Pro Ala Val His Arg Asp  
50 55 60

Met Ala Ala Arg Thr Ser Pro Leu Arg Pro Ile Val Ala Thr Thr Gly  
65 70 75 80

Pro Thr Leu Ser Pro Val Pro Pro Val Val His Leu Thr Leu Arg Arg  
85 90 95

Ala Gly Asp Asp Phe Ser Arg Arg Tyr Arg Arg Asp Phe Ala Glu Met  
100 105 110

Ser Ser Gln Leu His Leu Thr Pro Phe Thr Ala Arg Gly Arg Phe Ala  
115 120 125

Thr Val Val Glu Glu Leu Phe Arg Asp Gly Val Asn Trp Gly Arg Ile  
130 135 140

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Val Ala Phe Phe Glu Phe Gly Gly Val Met Cys Val Glu Ser Val Asn  
145 150 155 160

Arg Glu Met Ser Pro Leu Val Asp Asn Ile Ala Leu Trp Met Thr Glu  
165 170 175

Tyr Leu Asn Arg His Leu His Thr Trp Ile Gln Asp Asn Gly Gly Trp  
180 185 190

Asp Ala Phe Val Glu Leu Tyr Gly Pro Ser Val Arg Pro Leu Phe Asp  
195 200 205

Phe Ser Trp Leu Ser Leu Lys Thr Leu Leu Ser Leu Ala Leu Val Gly  
210 215 220

Ala Cys Ile Thr Leu Gly Thr Tyr Leu Gly His Lys  
225 230 235

<210> 2  
<211> 195  
<212> PRT  
<213> Cricetulus longicaudatus

<400> 2  
Met Ala Gln Ala Gly Arg Thr Gly Tyr Asp Asn Arg Glu Ile Val Met  
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Lys Tyr Ile His Tyr Lys Leu Ser Gln Arg Gly Tyr Glu Trp Asp Val  
20 25 30

Gly Asp Val Asp Ala Ala Ala Ala Ala Ser Pro Val Pro Pro Val  
35 40 45

Val His Leu Thr Leu Arg Arg Ala Gly Asp Asp Phe Ser Arg Arg Tyr  
50 55 60

Arg Arg Asp Phe Ala Glu Met Ser Ser Gln Leu His Leu Thr Pro Phe  
65 70 75 80

Thr Ala Arg Gly Arg Phe Ala Thr Val Val Glu Glu Leu Phe Arg Asp  
85 90 95

Gly Val Asn Trp Gly Arg Ile Val Ala Phe Phe Glu Phe Gly Gly Val  
100 105 110

Met Cys Val Glu Ser Val Asn Arg Glu Met Ser Pro Leu Val Asp Asn  
115 120 125

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Ile Ala Leu Trp Met Thr Glu Tyr Leu Asn Arg His Leu His Thr Trp  
130 135 140

Ile Gln Asp Asn Gly Gly Trp Asp Ala Phe Val Glu Leu Tyr Gly Pro  
145 150 155 160

Ser Val Arg Pro Leu Phe Asp Phe Ser Trp Leu Ser Leu Lys Thr Leu  
165 170 175

Leu Ser Leu Ala Leu Val Gly Ala Cys Ile Thr Leu Gly Thr Tyr Leu  
180 185 190

Gly His Lys  
195

<210> 3  
<211> 588  
<212> DNA  
<213> Cricetulus longicaudatus

<400> 3  
atggctcaag ctgggagaac agggtatgtat aaccgagaga tcgtgtatgaa gtacatccat 60  
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gccgcgagcc ccgtgccacc tgtggtccac ctgaccctcc gccgggctgg ggatgacttc 180  
tcccgtcgct accgtcgcga cttcgccggag atgtccagtc agctgcaccc tgcgccttc 240  
accgcgaggg gacgcgttgc tacggtggtg gaggaactct tcagggatgg ggtgaactgg 300  
gggaggattt tggccttctt tgagttcggt ggggtcatgt gtgtggagag cgtcaacagg 360  
gagatgtcac ccctggtgga caacatcgcc ctgtggatga ccgagttaccc gaaccggcat 420  
ctgcacaccc ggatccagga taacggaggc tgggacgcatttggact gtacggcccc 480  
agtgtgaggc ctctgtttga tttctttgg ctgtctctga agaccctgct cagcctggcc 540  
ctggtcgggg cctgcatcac tctgggtacc tacctgggcc acaagtga 588

<210> 4  
<211> 289  
<212> PRT  
<213> Human adenovirus type 5

<400> 4  
Met Arg His Ile Ile Cys His Gly Gly Val Ile Thr Glu Glu Met Ala  
1 5 10 15

Ala Ser Leu Leu Asp Gln Leu Ile Glu Glu Val Leu Ala Asp Asn Leu  
20 25 30

Pro Pro Pro Ser His Phe Glu Pro Pro Thr Leu His Glu Leu His Asp  
35 40 45

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Leu Asp Val Thr Ala Pro Glu Asp Pro Asn Glu Glu Ala Val Ser Gln  
50 55 60

Ile Phe Pro Asp Ser Val Met Leu Ala Val Gln Glu Gly Ile Asp Leu  
65 70 75 80

Leu Thr Phe Pro Pro Ala Pro Gly Ser Pro Glu Pro Pro His Leu Ser  
85 90 95

Arg Gln Pro Glu Gln Pro Glu Gln Arg Ala Leu Gly Pro Val Ser Met  
100 105 110

Pro Asn Leu Val Pro Glu Val Ile Asp Leu Thr Gly His Glu Ala Gly  
115 120 125

Phe Pro Pro Ser Asp Asp Glu Asp Glu Glu Gly Glu Glu Phe Val Leu  
130 135 140

Asp Tyr Val Glu His Pro Gly His Gly Cys Arg Ser Cys His Tyr His  
145 150 155 160

Arg Arg Asn Thr Gly Asp Pro Asp Ile Met Cys Ser Leu Cys Tyr Met  
165 170 175

Arg Thr Cys Gly Met Phe Val Tyr Ser Pro Val Ser Glu Pro Glu Pro  
180 185 190

Glu Pro Glu Pro Glu Pro Glu Pro Ala Arg Pro Thr Arg Arg Pro Lys  
195 200 205

Met Ala Pro Ala Ile Leu Arg Arg Pro Thr Ser Pro Val Ser Arg Glu  
210 215 220

Cys Asn Ser Ser Thr Asp Ser Cys Asp Ser Gly Pro Ser Asn Thr Pro  
225 230 235 240

Pro Glu Ile His Pro Val Val Pro Leu Cys Pro Ile Lys Pro Val Ala  
245 250 255

Val Arg Val Gly Gly Arg Arg Gln Ala Val Glu Cys Ile Glu Asp Leu  
260 265 270

Leu Asn Glu Pro Gly Gln Pro Leu Asp Leu Ser Cys Lys Arg Pro Arg  
275 280 285

Pro

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<210> 5  
<211> 986  
<212> DNA  
<213> Human adenovirus type 5

<400> 5  
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gaccagctga tcgaagaggt actggctgat aatcttccac ctccttagcca ttttgaacca 120  
cctacccttc acgaactgca tgatttagac gtgacggccc ccgaagatcc caacgaggag 180  
gcggtttcgc agattttcc cgactctgta atgttggcg tgcaggaagg gattgactta 240  
ctcactttc cgccggcgcc cggttctccg gagccgcctc accttcccg gcagcccgag 300  
cagccggagc agagagcctt gggtccgggt tctatgccaa accttgtacc ggaggtgatc 360  
gatcttaccg gccacgaggc tggcttcca cccagtgacg acgaggatga agagggtgag 420  
gagtttgtt tagattatgt ggagcaccccc gggcacgggt gcaggtctg tcattatcac 480  
cgaggagaata cgggggaccc agatattatg tggcgctt gctatatgag gacctgtggc 540  
atgttgtct acagtaagtg aaaattatgg gcagtgggt atagagtggg gggtttgggt 600  
tggtaatttt ttttttaatt tttacagttt tgtggtttaa agaattttgt attgtgattt 660  
ttttaaaagg tcctgtgtct gaacctgagc ctgagcccga gccagaaccg gagcctgcaa 720  
gacctacccg ccgtcctaaa atggcgccctg ctatcctgag acgcccgaca tcacctgtgt 780  
ctagagaatg caatagtagt acggatagct gtgactccgg tccttctaacc acacccctg 840  
agatacaccc ggtggtcccg ctgtgccccca tttaaaccagt tgccgtgaga gttggtgggc 900  
gtcgccaggc tggatgt atcgaggact tgcttaacga gcctgggcaa cctttggact 960  
tgagctgtaa acgccccagg ccataa 986

<210> 6  
<211> 39  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Description of Artificial Sequence: Synthetic primer

<400> 6  
cccgaaattcg ccgcccaccat gagacatatt atctgccac 39

<210> 7  
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<212> DNA  
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<220>

SequenceListing-73670826.txt  
<223> Description of Artificial sequence: Synthetic primer

<400> 7  
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28

<210> 8  
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<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial sequence: Synthetic primer

<400> 8  
cccggtaccg cccgcaccat gagacatatt atctgccac

39

<210> 9  
<211> 30  
<212> DNA  
<213> Artificial Sequence

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<223> Description of Artificial sequence: Synthetic primer

<400> 9  
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30

<210> 10  
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<212> DNA  
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<400> 10  
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25

<210> 11  
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<212> DNA  
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<220>  
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36

<210> 12  
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<212> DNA  
<213> Artificial Sequence

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<220>  
<223> Description of Artificial Sequence: Synthetic primer

<400> 12  
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<210> 13  
<211> 38  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence: Synthetic primer

<400> 13  
cccgaaattcg ccgccaccat ggaggcttgg gagtgttt 38

<210> 14  
<211> 29  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence: Synthetic primer

<400> 14  
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<210> 15  
<211> 558  
<212> DNA  
<213> Human adenovirus type 5

<400> 15  
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caggcaaagt tagtctgcag aattaaggag gattacaagt gggaaattga agagctttg 180  
aaatccgtg gtgagctgt tgattcttgc aatctgggtc accaggcgct tttccaagag 240  
aaggcatca agactttgaa ttttccaca ccggggcgcg ctgcggctgc tggctttt 300  
ttgagttta taaaggataa atggagcgaa gaaacccatc tgagcgaaaa gtacctgctg 360  
gattttctgg ccatgcatact gtggagagcg gttgtgagac acaagaatcg cctgctactg 420  
ttgtctccg tccgccccgc gataataccg acggaggagc agcagcagca gcaggagaa 480  
gccaggcgcc ggcggcagga gcagagccca tggaaaccga gagccggcct ggaccctcg 540  
gaatgaatgt tggtcgac 558

<210> 16

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<211> 38  
 <212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 16

cccgtcgacg ccgcccacat gccgccccaaa acccccccg

38

<210> 17

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 17

cccgcgcccg ccgggtcctga gatcctcatt tc

32

<210> 18

<211> 2824

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (16)..(2799)

<400> 18

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		1				5				10					

gcc	gcc	gct	gcc	gcc	gca	gaa	ccc	ccg	gca	ccg	ccg	ccg	ccc	cct		99
Ala	Ala	Ala	Ala	Ala	Glu	Pro	Pro	Ala	Pro	Pro	Pro	Pro	Pro	Pro		
15					20				25							

cct	gag	gag	gac	cca	gag	cag	gac	agc	ggc	ccg	gag	gac	ctg	cct	ctc		147
Pro	Glu	Glu	Asp	Pro	Glu	Gln	Asp	Ser	Gly	Pro	Glu	Asp	Leu	Pro	Leu		
30				35					40								

gtc	agg	ctt	gag	ttt	gaa	gaa	aca	gaa	gaa	cct	gat	ttt	act	gca	tta		195
Val	Arg	Leu	Glu	Phe	Glu	Glu	Thr	Glu	Glu	Pro	Asp	Phe	Thr	Ala	Leu		
45				50				55					60				

tgt	cag	aaa	tta	aag	ata	cca	gat	cat	gtc	aga	gag	aga	gct	tgg	tta		243
Cys	Gln	Lys	Leu	Lys	Ile	Pro	Asp	His	Val	Arg	Glu	Arg	Ala	Trp	Leu		
65					70				75								

act	tgg	gag	aaa	gtt	tca	tct	gtg	gat	gga	gta	ttg	gga	ggt	tat	att		291
Thr	Trp	Glu	Lys	Val	Ser	Ser	Val	Asp	Gly	Val	Leu	Gly	Gly	Tyr	Ile		
80					85					90							

caa	aag	aaa	aag	gaa	ctg	tgg	gga	atc	tgt	atc	ttt	att	gca	cga	gtt		339
Gln	Lys	Lys	Glu	Leu	Trp	Gly	Ile	Cys	Ile	Phe	Ile	Ala	Arg	Val			
95					100				105								

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gac cta gat gag atg tcg ttc act tta ctg agc tac aga aaa aca tac Asp Leu Asp Glu Met Ser Phe Thr Leu Leu Ser Tyr Arg Lys Thr Tyr 110 115 120	387
gaa atc agt gtc cat aaa ttc ttt aac tta cta aaa gaa att gat acc Glu Ile Ser Val His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp Thr 125 130 135 140	435
agt acc aaa gtt gat aat gct atg tca aga ctg ttg aag aag tat gat Ser Thr Lys Val Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr Asp 145 150 155	483
gta ttg ttt gca ctc ttc agc aaa ttg gaa agg aca tgt gaa ctt ata Val Leu Phe Ala Leu Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu Ile 160 165 170	531
tat ttg aca caa ccc agc agt tcg ata tct act gaa ata aat tct gca Tyr Leu Thr Gln Pro Ser Ser Ser Ile Ser Thr Glu Ile Asn Ser Ala 175 180 185	579
ttg gtg cta aaa gtt tct tgg atc aca ttt tta tta gct aaa ggg gaa Leu Val Leu Lys Val Ser Trp Ile Thr Phe Leu Leu Ala Lys Gly Glu 190 195 200	627
gta tta caa atg gaa gat gat ctg gtg att tca ttt cag tta atg cta Val Leu Gln Met Glu Asp Asp Leu Val Ile Ser Phe Gln Leu Met Leu 205 210 215 220	675
tgt gtc ctt gac tat ttt att aaa ctc tca cct ccc atg ttg ctc aaa Cys Val Leu Asp Tyr Phe Ile Lys Leu Ser Pro Pro Met Leu Leu Lys 225 230 235	723
gaa cca tat aaa aca gct gtt ata ccc att aat ggt tca cct cga aca Glu Pro Tyr Lys Thr Ala Val Ile Pro Ile Asn Gly Ser Pro Arg Thr 240 245 250	771
ccc agg cga ggt cag aac agg agt gca cgg ata gca aaa caa cta gaa Pro Arg Arg Gly Gln Asn Arg Ser Ala Arg Ile Ala Lys Gln Leu Glu 255 260 265	819
aat gat aca aga att att gaa gtt ctc tgt aaa gaa cat gaa tgt aat Asn Asp Thr Arg Ile Ile Glu Val Leu Cys Lys Glu His Glu Cys Asn 270 275 280	867
ata gat gag gtg aaa aat gtt tat ttc aaa aat ttt ata cct ttt atg Ile Asp Glu Val Lys Asn Val Tyr Phe Lys Asn Phe Ile Pro Phe Met 285 290 295 300	915
aat tct ctt gga ctt gta aca tct aat gga ctt cca gag gtt gaa aat Asn Ser Leu Gly Leu Val Thr Ser Asn Gly Leu Pro Glu Val Glu Asn 305 310 315	963
ctt tct aaa cga tac gaa gaa att tat ctt aaa aat aaa gat cta gat Leu Ser Lys Arg Tyr Glu Glu Ile Tyr Leu Lys Asn Lys Asp Leu Asp 320 325 330	1011
cga aga tta ttt ttg gat cat gat aaa act ctt cag act gat tct ata Arg Arg Leu Phe Leu Asp His Asp Lys Thr Leu Gln Thr Asp Ser Ile 335 340 345	1059
gac agt ttt gaa aca cag aga aca cca cga aaa agt aac ctt gat gaa Asp Ser Phe Glu Thr Gln Arg Thr Pro Arg Lys Ser Asn Leu Asp Glu	1107

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350	355	360															
gag	gtg	aat	ata	att	cct	cca	cac	act	cca	gtt	agg	act	gtt	atg	aac	1155	
Glu	Val	Asn	Ile	Ile	Pro	Pro	His	Thr	Pro	Val	Arg	Thr	Val	Met	Asn		
365				370					375					380			
act	atc	caa	caa	tta	atg	atg	att	tta	aat	tct	gca	agt	gat	caa	cct	1203	
Thr	Ile	Gln	Gln	Leu	Met	Met	Ile	Leu	Asn	Ser	Ala	Ser	Asp	Gln	Pro		
					385				390					395			
tca	gaa	aat	ctg	att	tcc	tat	ttt	aac	aac	tgc	aca	gtg	aat	cca	aaa	1251	
Ser	Glu	Asn	Leu	Ile	Ser	Tyr	Phe	Asn	Asn	Cys	Thr	Val	Asn	Pro	Lys		
					400			405				410					
gaa	agt	ata	ctg	aaa	aga	gtg	aag	gat	ata	gga	tac	atc	ttt	aaa	gag	1299	
Glu	Ser	Ile	Leu	Lys	Arg	Val	Lys	Asp	Ile	Gly	Tyr	Ile	Phe	Lys	Glu		
					415			420			425						
aaa	ttt	gct	aaa	gct	gtg	gga	cag	ggt	tgt	gtc	gaa	att	gga	tca	cag	1347	
Lys	Phe	Ala	Lys	Ala	Val	Gly	Gln	Gly	Cys	Val	Glu	Ile	Gly	Ser	Gln		
					430			435			440						
cga	tac	aaa	ctt	gga	gtt	cgc	ttg	tat	tac	cga	gta	atg	gaa	tcc	atg	1395	
Arg	Tyr	Lys	Leu	Gly	Val	Arg	Leu	Tyr	Tyr	Arg	Val	Met	Glu	Ser	Met		
					445			450			455			460			
ctt	aaa	tca	gaa	gaa	cga	tta	tcc	att	caa	aat	ttt	agc	aaa	ctt		1443	
Leu	Lys	Ser	Glu	Glu	Arg	Leu	Ser	Ile	Gln	Asn	Phe	Ser	Lys	Leu			
					465			470			475						
ctg	aat	gac	aac	att	ttt	cat	atg	tct	tta	ttg	gcg	tgc	gct	ctt	gag	1491	
Leu	Asn	Asp	Ile	Phe	His	Met	Ser	Leu	Leu	Ala	Cys	Ala	Leu	Glu			
					480			485			490						
gtt	gta	atg	gcc	aca	tat	agc	aga	agt	aca	tct	cag	aat	ctt	gat	tct	1539	
Val	Val	Met	Ala	Thr	Tyr	Ser	Arg	Ser	Thr	Ser	Gln	Asn	Leu	Asp	Ser		
					495			500			505						
gga	aca	gat	ttg	tct	ttc	cca	tgg	att	ctg	aat	gtg	ctt	aat	tta	aaa	1587	
Gly	Thr	Asp	Leu	Ser	Phe	Pro	Trp	Ile	Leu	Asn	Val	Leu	Asn	Leu	Lys		
					510			515			520						
gcc	ttt	gat	ttt	tac	aaa	gtg	atc	gaa	agt	ttt	atc	aaa	gca	gaa	ggc	1635	
Ala	Phe	Asp	Phe	Tyr	Lys	Val	Ile	Glu	Ser	Phe	Ile	Lys	Ala	Glu	Gly		
					525			530			535			540			
aac	ttg	aca	aga	gaa	atg	ata	aaa	cat	tta	gaa	cga	tgt	gaa	cat	cga	1683	
Asn	Leu	Thr	Arg	Glu	Met	Ile	Lys	His	Leu	Glu	Arg	Cys	Glu	His	Arg		
					545			550			555						
atc	atg	gaa	tcc	ctt	gca	tgg	ctc	tca	gat	tca	cct	tta	ttt	gat	ctt	1731	
Ile	Met	Glu	Ser	Leu	Ala	Trp	Leu	Ser	Asp	Ser	Pro	Leu	Phe	Asp	Leu		
					560			565			570						
att	aaa	caa	tca	aag	gac	cga	gaa	gga	cca	act	gat	cac	ctt	gaa	tct	1779	
Ile	Lys	Gln	Ser	Lys	Asp	Arg	Glu	Gly	Pro	Thr	Asp	His	Leu	Glu	Ser		
					575			580			585						
gct	tgt	cct	ctt	aat	ctt	cct	ctc	cag	aat	aat	cac	act	gca	gca	gat	1827	
Ala	Cys	Pro	Leu	Asn	Leu	Pro	Leu	Gln	Asn	Asn	His	Thr	Ala	Ala	Asp		
					590			595			600						
atg	tat	ctt	tct	cct	gta	aga	tct	cca	aag	aaa	aaa	ggt	tca	act	acg	1875	

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Met Tyr Leu Ser Pro Val Arg Ser Pro Lys Lys Lys Gly Ser Thr Thr			
605	610	615	620
cgt gta aat tct act gca aat gca gag aca caa gca acc tca gcc ttc			1923
Arg Val Asn Ser Thr Ala Asn Ala Glu Thr Gln Ala Thr Ser Ala Phe			
625	630	635	
cag acc cag aag cca ttg aaa tct acc tct ctt tca ctg ttt tat aaa			1971
Gln Thr Gln Lys Pro Leu Lys Ser Thr Ser Leu Ser Leu Phe Tyr Lys			
640	645	650	
aaa gtg tat cgg cta gcc tat ctc cgg cta aat aca ctt tgt gaa cgc			2019
Lys Val Tyr Arg Leu Ala Tyr Leu Arg Leu Asn Thr Leu Cys Glu Arg			
655	660	665	
ctt ctg tct gag cac cca gaa tta gaa cat atc atc tgg acc ctt ttc			2067
Leu Leu Ser Glu His Pro Glu Leu Glu His Ile Ile Trp Thr Leu Phe			
670	675	680	
cag cac acc ctg cag aat gag tat gaa ctc atg aga gac agg cat ttg			2115
Gln His Thr Leu Gln Asn Glu Tyr Glu Leu Met Arg Asp Arg His Leu			
685	690	695	700
gac caa att atg atg tgt tcc atg tat ggc ata tgc aaa gtg aag aat			2163
Asp Gln Ile Met Met Cys Ser Met Tyr Gly Ile Cys Lys Val Lys Asn			
705	710	715	
ata gac ctt aaa ttc aaa atc att gta aca gca tac aag gat ctt cct			2211
Ile Asp Leu Lys Phe Lys Ile Ile Val Thr Ala Tyr Lys Asp Leu Pro			
720	725	730	
cat gct gtt cag gag aca ttc aaa cgt gtt ttg atc aaa gaa gag gag			2259
His Ala Val Gln Glu Thr Phe Lys Arg Val Leu Ile Lys Glu Glu Glu			
735	740	745	
tat gat tct att ata gta ttc tat aac tcg gtc ttc atg cag aga ctg			2307
Tyr Asp Ser Ile Ile Val Phe Tyr Asn Ser Val Phe Met Gln Arg Leu			
750	755	760	
aaa aca aat att ttg cag tat gct tcc acc agg ccc cct acc ttg tca			2355
Lys Thr Asn Ile Leu Gin Tyr Ala Ser Thr Arg Pro Pro Thr Leu Ser			
765	770	775	780
cca ata cct cac att cct cga agc cct tac aag ttt cct agt tca ccc			2403
Pro Ile Pro His Ile Pro Arg Ser Pro Tyr Lys Phe Pro Ser Ser Pro			
785	790	795	
tta cgg att cct gga ggg aac atc tat att tca ccc ctg aag agt cca			2451
Leu Arg Ile Pro Gly Gly Asn Ile Tyr Ile Ser Pro Leu Lys Ser Pro			
800	805	810	
tat aaa att tca gaa ggt ctg cca aca cca aca aaa atg act cca aga			2499
Tyr Lys Ile Ser Glu Gly Leu Pro Thr Pro Thr Lys Met Thr Pro Arg			
815	820	825	
tca aga atc tta gta tca att ggt gaa tca ttc ggg act tct gag aag			2547
Ser Arg Ile Leu Val Ser Ile Gly Glu Ser Phe Gly Thr Ser Glu Lys			
830	835	840	
ttc cag aaa ata aat cag atg gta tgt aac agc gac cgt gtg ctc aaa			2595
Phe Gln Lys Ile Asn Gln Met Val Cys Asn Ser Asp Arg Val Leu Lys			
845	850	855	860

SequenceListing-73670826.txt

aga agt gct gaa gga agc aac cct cct aaa cca ctg aaa aaa cta cgc Arg Ser Ala Glu Gly Ser Asn Pro Pro Lys Pro Leu Lys Lys Leu Arg 865 870 875	2643
ttt gat att gaa gga tca gat gaa gca gat gga agt aaa cat ctc cca Phe Asp Ile Glu Gly Ser Asp Glu Ala Asp Gly Ser Lys His Leu Pro 880 885 890	2691
gga gag tcc aaa ttt cag cag aaa ctg gca gaa atg act tct act cga Gly Glu Ser Lys Phe Gln Gln Lys Leu Ala Glu Met Thr Ser Thr Arg 895 900 905	2739
aca cga atg caa aag cag aaa atg aat gat agc atg gat acc tca aac Thr Arg Met Gln Lys Gln Lys Met Asn Asp Ser Met Asp Thr Ser Asn 910 915 920	2787
aag gaa gag aaa tgaggatctc aggaccggcg gccgc Lys Glu Glu Lys 925	2824
<210> 19	
<211> 928	
<212> PRT	
<213> Homo sapiens	
<400> 19	
Met Pro Pro Lys Thr Pro Arg Lys Thr Ala Ala Thr Ala Ala Ala Ala 1 5 10 15	
Ala Ala Glu Pro Pro Ala Pro Pro Pro Pro Pro Pro Pro Glu Glu Asp 20 25 30	
Pro Glu Gln Asp Ser Gly Pro Glu Asp Leu Pro Leu Val Arg Leu Glu 35 40 45	
Phe Glu Glu Thr Glu Glu Pro Asp Phe Thr Ala Leu Cys Gln Lys Leu 50 55 60	
Lys Ile Pro Asp His Val Arg Glu Arg Ala Trp Leu Thr Trp Glu Lys 65 70 75 80	
Val Ser Ser Val Asp Gly Val Leu Gly Gly Tyr Ile Gln Lys Lys Lys 85 90 95	
Glu Leu Trp Gly Ile Cys Ile Phe Ile Ala Arg Val Asp Leu Asp Glu 100 105 110	
Met Ser Phe Thr Leu Leu Ser Tyr Arg Lys Thr Tyr Glu Ile Ser Val 115 120 125	
His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp Thr Ser Thr Lys Val 130 135 140	

SequenceListing-73670826.txt

Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr Asp Val Leu Phe Ala  
145 150 155 160

Leu Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu Ile Tyr Leu Thr Gln  
165 170 175

Pro Ser Ser Ser Ile Ser Thr Glu Ile Asn Ser Ala Leu Val Leu Lys  
180 185 190

Val Ser Trp Ile Thr Phe Leu Leu Ala Lys Gly Glu Val Leu Gln Met  
195 200 205

Glu Asp Asp Leu Val Ile Ser Phe Gln Leu Met Leu Cys Val Leu Asp  
210 215 220

Tyr Phe Ile Lys Leu Ser Pro Pro Met Leu Leu Lys Glu Pro Tyr Lys  
225 230 235 240

Thr Ala Val Ile Pro Ile Asn Gly Ser Pro Arg Thr Pro Arg Arg Gly  
245 250 255

Gln Asn Arg Ser Ala Arg Ile Ala Lys Gln Leu Glu Asn Asp Thr Arg  
260 265 270

Ile Ile Glu Val Leu Cys Lys Glu His Glu Cys Asn Ile Asp Glu Val  
275 280 285

Lys Asn Val Tyr Phe Lys Asn Phe Ile Pro Phe Met Asn Ser Leu Gly  
290 295 300

Leu Val Thr Ser Asn Gly Leu Pro Glu Val Glu Asn Leu Ser Lys Arg  
305 310 315 320

Tyr Glu Glu Ile Tyr Leu Lys Asn Lys Asp Leu Asp Arg Arg Leu Phe  
325 330 335

Leu Asp His Asp Lys Thr Leu Gln Thr Asp Ser Ile Asp Ser Phe Glu  
340 345 350

Thr Gln Arg Thr Pro Arg Lys Ser Asn Leu Asp Glu Glu Val Asn Ile  
355 360 365

Ile Pro Pro His Thr Pro Val Arg Thr Val Met Asn Thr Ile Gln Gln  
370 375 380

Leu Met Met Ile Leu Asn Ser Ala Ser Asp Gln Pro Ser Glu Asn Leu  
385 390 395 400

SequenceListing-73670826.txt

Ile Ser Tyr Phe Asn Asn Cys Thr Val Asn Pro Lys Glu Ser Ile Leu  
405 410 415

Lys Arg Val Lys Asp Ile Gly Tyr Ile Phe Lys Glu Lys Phe Ala Lys  
420 425 430

Ala Val Gly Gln Gly Cys Val Glu Ile Gly Ser Gln Arg Tyr Lys Leu  
435 440 445

Gly Val Arg Leu Tyr Tyr Arg Val Met Glu Ser Met Leu Lys Ser Glu  
450 455 460

Glu Glu Arg Leu Ser Ile Gln Asn Phe Ser Lys Leu Leu Asn Asp Asn  
465 470 475 480

Ile Phe His Met Ser Leu Leu Ala Cys Ala Leu Glu Val Val Met Ala  
485 490 495

Thr Tyr Ser Arg Ser Thr Ser Gln Asn Leu Asp Ser Gly Thr Asp Leu  
500 505 510

Ser Phe Pro Trp Ile Leu Asn Val Leu Asn Leu Lys Ala Phe Asp Phe  
515 520 525

Tyr Lys Val Ile Glu Ser Phe Ile Lys Ala Glu Gly Asn Leu Thr Arg  
530 535 540

Glu Met Ile Lys His Leu Glu Arg Cys Glu His Arg Ile Met Glu Ser  
545 550 555 560

Leu Ala Trp Leu Ser Asp Ser Pro Leu Phe Asp Leu Ile Lys Gln Ser  
565 570 575

Lys Asp Arg Glu Gly Pro Thr Asp His Leu Glu Ser Ala Cys Pro Leu  
580 585 590

Asn Leu Pro Leu Gln Asn Asn His Thr Ala Ala Asp Met Tyr Leu Ser  
595 600 605

Pro Val Arg Ser Pro Lys Lys Lys Gly Ser Thr Thr Arg Val Asn Ser  
610 615 620

Thr Ala Asn Ala Glu Thr Gln Ala Thr Ser Ala Phe Gln Thr Gln Lys  
625 630 635 640

Pro Leu Lys Ser Thr Ser Leu Ser Leu Phe Tyr Lys Lys Val Tyr Arg  
645 650 655

SequenceListing-73670826.txt

Leu Ala Tyr Leu Arg Leu Asn Thr Leu Cys Glu Arg Leu Leu Ser Glu  
660 665 670

His Pro Glu Leu Glu His Ile Ile Trp Thr Leu Phe Gln His Thr Leu  
675 680 685

Gln Asn Glu Tyr Glu Leu Met Arg Asp Arg His Leu Asp Gln Ile Met  
690 695 700

Met Cys Ser Met Tyr Gly Ile Cys Lys Val Lys Asn Ile Asp Leu Lys  
705 710 715 720

Phe Lys Ile Ile Val Thr Ala Tyr Lys Asp Leu Pro His Ala Val Gln  
725 730 735

Glu Thr Phe Lys Arg Val Leu Ile Lys Glu Glu Glu Tyr Asp Ser Ile  
740 745 750

Ile Val Phe Tyr Asn Ser Val Phe Met Gln Arg Leu Lys Thr Asn Ile  
755 760 765

Leu Gln Tyr Ala Ser Thr Arg Pro Pro Thr Leu Ser Pro Ile Pro His  
770 775 780

Ile Pro Arg Ser Pro Tyr Lys Phe Pro Ser Ser Pro Leu Arg Ile Pro  
785 790 795 800

Gly Gly Asn Ile Tyr Ile Ser Pro Leu Lys Ser Pro Tyr Lys Ile Ser  
805 810 815

Glu Gly Leu Pro Thr Pro Thr Lys Met Thr Pro Arg Ser Arg Ile Leu  
820 825 830

Val Ser Ile Gly Glu Ser Phe Gly Thr Ser Glu Lys Phe Gln Lys Ile  
835 840 845

Asn Gln Met Val Cys Asn Ser Asp Arg Val Leu Lys Arg Ser Ala Glu  
850 855 860

Gly Ser Asn Pro Pro Lys Pro Leu Lys Lys Leu Arg Phe Asp Ile Glu  
865 870 875 880

Gly Ser Asp Glu Ala Asp Gly Ser Lys His Leu Pro Gly Glu Ser Lys  
885 890 895

Phe Gln Gln Lys Leu Ala Glu Met Thr Ser Thr Arg Thr Arg Met Gln

SequenceListing-73670826.txt  
 900                    905                    910

Lys Gln Lys Met Asn Asp Ser Met Asp Thr Ser Asn Lys Glu Glu Lys  
 915                    920                    925

<210> 20  
 <211> 1010  
 <212> DNA  
 <213> Rattus sp.

<220>  
 <221> CDS  
 <222> (16)..(996)

<400> 20

gaattcgccg ccacc atg acc atg gac tct gga gca gac aac cag cag agt	51
Met Thr Met Asp Ser Gly Ala Asp Asn Gln Gln Ser	
1                        5                        10	

gga gat gca gct gta aca gaa gct gaa aac caa caa atg aca gtt caa	99
Gly Asp Ala Ala Val Thr Glu Ala Glu Asn Gln Gln Met Thr Val Gln	
15                      20                        25	

gcc cag cca cag att gcc aca tta gcc cag gta tct atg cca gca gct	147
Ala Gln Pro Gln Ile Ala Thr Leu Ala Gln Val Ser Met Pro Ala Ala	
30                      35                        40	

cat gca aca tca tct gct ccc acc gta act cta gta cag ctg ccc aat	195
His Ala Thr Ser Ser Ala Pro Thr Val Thr Leu Val Gln Leu Pro Asn	
45                      50                        55                        60	

ggg cag aca gtt caa gtc cat gga gtc att cag gcg gcc cag cca tca	243
Gly Gln Thr Val Gln Val His Gly Val Ile Gln Ala Ala Gln Pro Ser	
65                      70                        75	

gtt att cag tct cca caa gtc caa aca gtt cag att tca act att gca	291
Val Ile Gln Ser Pro Gln Val Gln Thr Val Gln Ile Ser Thr Ile Ala	
80                      85                        90	

gaa agt gaa gat tca cag gag tca gtg gat agt gta act gat tcc caa	339
Glu Ser Glu Asp Ser Gln Glu Ser Val Asp Ser Val Thr Asp Ser Gln	
95                      100                        105	

aag cga agg gaa att ctt tca agg agg cct tcc ttc agg aaa att ttg	387
Lys Arg Arg Glu Ile Leu Ser Arg Arg Pro Ser Phe Arg Lys Ile Leu	
110                      115                        120	

aat gac tta tct tct gat gca cca gga gtg cca agg att gaa gaa gag	435
Asn Asp Leu Ser Ser Asp Ala Pro Gly Val Pro Arg Ile Glu Glu Glu	
125                      130                        135                        140	

aag tct gaa gag gag gct tca gca cct gcc atc acc gct gta gcg gtg	483
Lys Ser Glu Glu Ala Ser Ala Pro Ala Ile Thr Ala Val Ala Val	
145                      150                        155	

cca acg cca att tac cgg act agc agt gga cag tat att acc att acc	531
Pro Thr Pro Ile Tyr Arg Thr Ser Ser Gly Gln Tyr Ile Thr Ile Thr	
160                      165                        170	

cag aga gga gca ata cag ctg gct agc aat ggt acc gat ggg gta cag	579
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SequenceListing-73670826.txt

Gln Arg Gly Ala Ile Gln Leu Ala Ser Asn Gly Thr Asp Gly Val Gln 175 180 185	
ggc ctg caa aca tta acc atg gcc aat gca gca gcc act cag ccg ggt Gly Leu Gln Thr Leu Thr Met Ala Asn Ala Ala Thr Gln Pro Gly 190 195 200	627
act acc att cta cag tat gca cag acc act gat gga cag cag atc tta Thr Thr Ile Leu Gln Tyr Ala Gln Thr Thr Asp Gly Gln Gln Ile Leu 205 210 215 220	675
gtg ccc agc aac caa gtt gtt gtt caa gct gcc tct gga gac gta caa Val Pro Ser Asn Gln Val Val Val Gln Ala Ala Ser Gly Asp Val Gln 225 230 235	723
aca tac cag att cgc aca gca ccc act agc act att gcc cct gga gtt Thr Tyr Gln Ile Arg Thr Ala Pro Thr Ser Thr Ile Ala Pro Gly Val 240 245 250	771
gtt atg gca tcc tcc cca gca ctt cct aca cag cct gct gaa gaa gca Val Met Ala Ser Ser Pro Ala Leu Pro Thr Gln Pro Ala Glu Glu Ala 255 260 265	819
gca cga aag aga gag gtc cgt cta atg aag aac agg gaa gca gct cgt Ala Arg Lys Arg Glu Val Arg Leu Met Lys Asn Arg Glu Ala Ala Arg 270 275 280	867
gag tgt cgt aga aag aag aaa gaa tat gtg aaa tgt tta gaa aac aga Glu Cys Arg Arg Lys Lys Glu Tyr Val Lys Cys Leu Glu Asn Arg 285 290 295 300	915
gtg gca gtg ctt gaa aat caa aac aag aca ttg att gag gag cta aaa Val Ala Val Leu Glu Asn Gln Asn Lys Thr Leu Ile Glu Glu Leu Lys 305 310 315	963
gca ctt aag gac ctt tac tgc cac aaa tca gat taatttgggt cgac Ala Leu Lys Asp Leu Tyr Cys His Lys Ser Asp 320 325	1010

<210> 21  
<211> 327  
<212> PRT  
<213> Rattus sp.

<400> 21  
Met Thr Met Asp Ser Gly Ala Asp Asn Gln Gln Ser Gly Asp Ala Ala  
1 5 10 15

Val Thr Glu Ala Glu Asn Gln Gln Met Thr Val Gln Ala Gln Pro Gln  
20 25 30

Ile Ala Thr Leu Ala Gln Val Ser Met Pro Ala Ala His Ala Thr Ser  
35 40 45

Ser Ala Pro Thr Val Thr Leu Val Gln Leu Pro Asn Gly Gln Thr Val  
50 55 60

Gln Val His Gly Val Ile Gln Ala Ala Gln Pro Ser Val Ile Gln Ser

65

70

## SequenceListing-73670826.txt

75

80

Pro Gln Val Gln Thr Val Gln Ile Ser Thr Ile Ala Glu Ser Glu Asp  
85 90 95

Ser Gln Glu Ser Val Asp Ser Val Thr Asp Ser Gln Lys Arg Arg Glu  
100 105 110

Ile Leu Ser Arg Arg Pro Ser Phe Arg Lys Ile Leu Asn Asp Leu Ser  
115 120 125

Ser Asp Ala Pro Gly Val Pro Arg Ile Glu Glu Lys Ser Glu Glu  
130 135 140

Glu Ala Ser Ala Pro Ala Ile Thr Ala Val Ala Val Pro Thr Pro Ile  
145 150 155 160

Tyr Arg Thr Ser Ser Gly Gln Tyr Ile Thr Ile Thr Gln Arg Gly Ala  
165 170 175

Ile Gln Leu Ala Ser Asn Gly Thr Asp Gly Val Gln Gly Leu Gln Thr  
180 185 190

Leu Thr Met Ala Asn Ala Ala Ala Thr Gln Pro Gly Thr Thr Ile Leu  
195 200 205

Gln Tyr Ala Gln Thr Thr Asp Gly Gln Gln Ile Leu Val Pro Ser Asn  
210 215 220

Gln Val Val Val Gln Ala Ala Ser Gly Asp Val Gln Thr Tyr Gln Ile  
225 230 235 240

Arg Thr Ala Pro Thr Ser Thr Ile Ala Pro Gly Val Val Met Ala Ser  
245 250 255

Ser Pro Ala Leu Pro Thr Gln Pro Ala Glu Glu Ala Ala Arg Lys Arg  
260 265 270

Glu Val Arg Leu Met Lys Asn Arg Glu Ala Ala Arg Glu Cys Arg Arg  
275 280 285

Lys Lys Lys Glu Tyr Val Lys Cys Leu Glu Asn Arg Val Ala Val Leu  
290 295 300

Glu Asn Gln Asn Lys Thr Leu Ile Glu Glu Leu Lys Ala Leu Lys Asp  
305 310 315 320

SequenceListing-73670826.txt  
Leu Tyr Cys His Lys Ser Asp  
325

<210> 22

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 22

cccgaaattcgc cccgcaccat gaccatggac tctggagcag aca

43

<210> 23

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 23

gtcgacccaa attaatctga tttgtggcag

30

<210> 24

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 24

gtcaagcaag cttgccgcca ccatgagaca tattatctgc cacgg

45

<210> 25

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 25

cgcagtctcg agttatggcc tggggcgttt acagctc

37

<210> 26

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

SequenceListing-73670826.txt

primer

<400> 26  
cacctaccct tcacgaactg catgatTTAG acgtgacggc c 41

<210> 27  
<211> 41  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic primer

<400> 27  
ggccgtcACG tctaaATcat gcagttcgtg aaggtaggt g 41

<210> 28  
<211> 42  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic primer

<400> 28  
cgaggGTGAT cgatCTTacc ggccACGagg ctggCTTcc ac 42

<210> 29  
<211> 42  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic primer

<400> 29  
gtggAAAGCC agcCTCGTGG ccggtaAGAT cgatCACCTC CG 42

<210> 30  
<211> 42  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic primer

<400> 30  
gtcaAGCAAG ctTGCCTCCA ccatGACCAT ggaATCTGGA GC 42

<210> 31  
<211> 37  
<212> DNA  
<213> Artificial Sequence

SequenceListing-73670826.txt

<220>  
<223> Description of Artificial Sequence: synthetic  
primer

<400> 31  
cgcagtggat ccttaatctg atttgtggca gtaaagg 37

<210> 32  
<211> 39  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: synthetic  
primer

<400> 32  
gtcattcaaa atttcctga aggaaggcct ccttgaaag 39

<210> 33  
<211> 40  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
primer

<400> 33  
tcttcaagg aggcccttcct tcagaaaaat tttgaatgac 40

<210> 34  
<211> 57  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
primer

<400> 34  
ggcattccaa gcttactgtt ggtaaagccg ccaccatgga ggcttggag tgtttgg 57

<210> 35  
<211> 36  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
primer

<400> 35  
gatcgactct agatcattcc cgagggtcca ggccgg 36

<210> 36  
<211> 38  
<212> DNA

SequenceListing-73670826.txt

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
primer

<400> 36

taaagccacc atggctcaag ctgggagaac agggtatg

38

<210> 37

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
primer

<400> 37

gatcgactct agatcacttg tggcccaggt aggtaccc

38

<210> 38

<211> 55

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
primer

<400> 38

gtgggagatg tggacgcccc ggccgcggcc gcgagccccc tgccacctgt ggtcc

55

<210> 39

<211> 55

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
primer

<400> 39

ggaccacagg tggcacgggg ctcgcggccg cggccgcggc gtccacatct cccac

55

<210> 40

<211> 891

<212> DNA

<213> Human adenovirus type 5

<220>

<221> CDS

<222> (16)..(882)

<400> 40

aagcttgcgg ccacc atg aga cat att atc tgc cac gga ggt gtt att acc  
Met Arg His Ile Ile Cys His Gly Gly Val Ile Thr  
1 5 10

51

SequenceListing-73670826.txt

gaa gaa atg gcc gcc agt ctt ttg gac cag ctg atc gaa gag gta ctg Glu Glu Met Ala Ala Ser Leu Leu Asp Gln Leu Ile Glu Glu Val Leu 15 20 25	99
gct gat aat ctt cca cct cct agc cat ttt gaa cca cct acc ctt cac Ala Asp Asn Leu Pro Pro Ser His Phe Glu Pro Pro Thr Leu His 30 35 40	147
gaa ctg tat gat tta gac gtg acg gcc ccc gaa gat ccc aac gag gag Glu Leu Tyr Asp Leu Asp Val Thr Ala Pro Glu Asp Pro Asn Glu Glu 45 50 55 60	195
gcg gtt tcg cag att ttt ccc gac tct gta atg ttg gcg gtg cag gaa Ala Val Ser Gln Ile Phe Pro Asp Ser Val Met Leu Ala Val Gln Glu 65 70 75	243
ggg att gac tta ctc act ttt ccg ccg gcg ccc ggt tct ccg gag ccg Gly Ile Asp Leu Leu Thr Phe Pro Pro Ala Pro Gly Ser Pro Glu Pro 80 85 90	291
cct cac ctt tcc cgg cag ccc gag cag ccg gag cag aga gcc ttg ggt Pro His Leu Ser Arg Gln Pro Glu Gln Pro Glu Gln Arg Ala Leu Gly 95 100 105	339
ccg gtt tct atg cca aac ctt gta ccg gag gtg atc gat ctt acc tgc Pro Val Ser Met Pro Asn Leu Val Pro Glu Val Ile Asp Leu Thr Cys 110 115 120	387
cac gag gct ggc ttt cca ccc agt gac gac gag gat gaa gag ggt gag His Glu Ala Gly Phe Pro Pro Ser Asp Asp Glu Asp Glu Glu Gly Glu 125 130 135 140	435
gag ttt gtg tta gat tat gtg gag cac ccc ggg cac ggt tgc agg tct Glu Phe Val Leu Asp Tyr Val Glu His Pro Gly His Gly Cys Arg Ser 145 150 155	483
tgt cat tat cac cgg agg aat acg ggg gac cca gat att atg tgt tgc Cys His Tyr His Arg Arg Asn Thr Gly Asp Pro Asp Ile Met Cys Ser 160 165 170	531
ctt tgc tat atg agg acc tgt ggc atg ttt gtc tac agt cct gtg tct Leu Cys Tyr Met Arg Thr Cys Gly Met Phe Val Tyr Ser Pro Val Ser 175 180 185	579
gaa cct gag cct gag ccc gag cca gaa ccg gag cct gca aga cct acc Glu Pro Glu Pro Glu Pro Glu Pro Glu Pro Ala Arg Pro Thr 190 195 200	627
cgc cgt cct aaa atg gcg cct gct atc ctg aga cgc ccg aca tca cct Arg Arg Pro Lys Met Ala Pro Ala Ile Leu Arg Arg Pro Thr Ser Pro 205 210 215 220	675
gtg tct aga gaa tgc aat agt agt acg gat agc tgt gac tcc ggt cct Val Ser Arg Glu Cys Asn Ser Ser Thr Asp Ser Cys Asp Ser Gly Pro 225 230 235	723
tct aac aca cct cct gag ata cac ccg gtg gtc ccg ctg tgc ccc att Ser Asn Thr Pro Pro Glu Ile His Pro Val Val Pro Leu Cys Pro Ile 240 245 250	771
aaa cca gtt gcc gtg aga gtt ggt ggg cgt cgc cag gct gtg gaa tgt Lys Pro Val Ala Val Arg Val Gly Gly Arg Arg Gln Ala Val Glu Cys	819

SequenceListing-73670826.txt  
260                    265

atc gag gac ttg ctt aac gag cct ggg caa cct ttg gac ttg agc tgt Ile Glu Asp Leu Leu Asn Glu Pro Gly Gln Pro Leu Asp Leu Ser Cys 270                    275                    280	867
aaa cgc ccc agg cca taactcgag Lys Arg Pro Arg Pro 285	891
 <b>&lt;210&gt; 41</b>	
<b>&lt;211&gt; 891</b>	
<b>&lt;212&gt; DNA</b>	
<b>&lt;213&gt; Human adenovirus type 5</b>	
 <b>&lt;220&gt;</b>	
<b>&lt;221&gt; CDS</b>	
<b>&lt;222&gt; (16)..(882)</b>	
 <b>&lt;400&gt; 41</b>	
aagcttgccg ccacc atg aga cat att atc tgc cac gga ggt gtt att acc Met Arg His Ile Ile Cys His Gly Gly Val Ile Thr 1                    5                    10	51
gaa gaa atg gcc gcc agt ctt ttg gac cag ctg atc gaa gag gta ctg Glu Glu Met Ala Ala Ser Leu Leu Asp Gln Leu Ile Glu Glu Val Leu 15                    20                    25	99
gct gat aat ctt cca cct cct agc cat ttt gaa cca cct acc ctt cac Ala Asp Asn Leu Pro Pro Ser His Phe Glu Pro Pro Thr Leu His 30                    35                    40	147
gaa ctg cat gat tta gac gtg acg gcc ccc gaa gat ccc aac gag gag Glu Leu His Asp Leu Asp Val Thr Ala Pro Glu Asp Pro Asn Glu Glu 45                    50                    55                    60	195
gcg gtt tcg cag att ttt ccc gac tct gta atg ttg gcg gtg cag gaa Ala Val Ser Gln Ile Phe Pro Asp Ser Val Met Leu Ala Val Gln Glu 65                    70                    75	243
ggg att gac tta ctc act ttt ccg ccg gcg ccc ggt tct ccg gag ccg Gly Ile Asp Leu Leu Thr Phe Pro Pro Ala Pro Gly Ser Pro Glu Pro 80                    85                    90	291
cct cac ctt tcc ccg cag ccc gag cag ccg gag cag aga gcc ttg ggt Pro His Leu Ser Arg Gln Pro Glu Gln Pro Glu Gln Arg Ala Leu Gly 95                    100                    105	339
ccg gtt tct atg cca aac ctt gta ccg gag gtg atc gat ctt acc tgc Pro Val Ser Met Pro Asn Leu Val Pro Glu Val Ile Asp Leu Thr Cys 110                    115                    120	387
cac gag gct ggc ttt cca ccc agt gac gag gag gat gaa gag ggt gag His Glu Ala Gly Phe Pro Pro Ser Asp Asp Glu Asp Glu Glu Gly Glu 125                    130                    135                    140	435
gag ttt gtg tta gat tat gtg gag cac ccc ggg cac ggt tgc agg tct Glu Phe Val Leu Asp Tyr Val Glu His Pro Gly His Gly Cys Arg Ser 145                    150                    155	483
tgt cat tat cac ccg agg aat acg ggg gac cca gat att atg tgt tcg	531

SequenceListing-73670826.txt

Cys His Tyr His Arg Arg Asn Thr Gly Asp Pro Asp Ile Met Cys Ser			
160	165	170	
ctt tgc tat atg agg acc tgt ggc atg ttt gtc tac agt cct gtg tct	579		
Leu Cys Tyr Met Arg Thr Cys Gly Met Phe Val Tyr Ser Pro Val Ser			
175	180	185	
gaa cct gag cct gag ccc gag cca gaa ccg gag cct gca aga cct acc	627		
Glu Pro Glu Pro Glu Pro Glu Pro Glu Pro Ala Arg Pro Thr			
190	195	200	
cgc cgt cct aaa atg gcg cct gct atc ctg aga cgc ccg aca tca cct	675		
Arg Arg Pro Lys Met Ala Pro Ala Ile Leu Arg Arg Pro Thr Ser Pro			
205	210	215	220
gtg tct aga gaa tgc aat agt agt acg gat agc tgt gac tcc ggt cct	723		
Val Ser Arg Glu Cys Asn Ser Ser Thr Asp Ser Cys Asp Ser Gly Pro			
225	230	235	
tct aac aca cct cct gag ata cac ccg gtg gtc ccg ctg tgc ccc att	771		
Ser Asn Thr Pro Pro Glu Ile His Pro Val Val Pro Leu Cys Pro Ile			
240	245	250	
aaa cca gtt gcc gtg aga gtt ggt ggg cgt cgc cag gct gtg gaa tgt	819		
Lys Pro Val Ala Val Arg Val Gly Gly Arg Arg Gln Ala Val Glu Cys			
255	260	265	
atc gag gac ttg ctt aac gag cct ggg caa cct ttg gac ttg agc tgt	867		
Ile Glu Asp Leu Leu Asn Glu Pro Gly Gln Pro Leu Asp Leu Ser Cys			
270	275	280	
aaa cgc ccc agg cca taactcgag	891		
Lys Arg Pro Arg Pro			
285			

<210> 42  
<211> 1047  
<212> DNA  
<213> Cricetulus longicaudatus

<220>			
<221> CDS			
<222> (16)..(1038)			
<400> 42			
aagcttgccg ccacc atg acc atg gaa tct gga gca gac aac cag cag agt	51		
Met Thr Met Glu Ser Gly Ala Asp Asn Gln Gln Ser			
1	5	10	
gga gat gct gta aca gaa gct gaa aat caa caa atg aca gct caa	99		
Gly Asp Ala Ala Val Thr Glu Ala Glu Asn Gln Gln Met Thr Ala Gln			
15	20	25	
gcc caa cca cag att gcc aca tta gcc cag gta tcc atg cca gca gct	147		
Ala Gln Pro Gln Ile Ala Thr Leu Ala Gln Val Ser Met Pro Ala Ala			
30	35	40	
cat gcg aca tca tct gct ccc act gta acc tta gtg cag ctg ccc aat	195		
His Ala Thr Ser Ser Ala Pro Thr Val Thr Leu Val Gln Leu Pro Asn			
45	50	55	60

SequenceListing-73670826.txt

ggg cag aca gtc caa gtc cat gga gtt att cag gcg gcc cag cca tca Gly Gln Thr Val Gln Val His Gly Val Ile Gln Ala Ala Gln Pro Ser 65 70 75	243
gtt att cag tct cca caa gtc caa aca gtt cag tct tcc tgt aag gac Val Ile Gln Ser Pro Gln Val Gln Thr Val Gln Ser Ser Cys Lys Asp 80 85 90	291
tta aaa aga ctt ttc tcc gga act cag att tca act att gca gaa agt Leu Lys Arg Leu Phe Ser Gly Thr Gln Ile Ser Thr Ile Ala Glu Ser 95 100 105	339
gag gat tca cag gaa tct gtg gat agt gta act gat tcc caa aag cga Glu Asp Ser Gln Glu Ser Val Asp Ser Val Thr Asp Ser Gln Lys Arg 110 115 120	387
agg gaa att ctt tca agg agg cct tcc tac agg aaa att ttg aat gac Arg Glu Ile Leu Ser Arg Arg Pro Ser Tyr Arg Lys Ile Leu Asn Asp 125 130 135 140	435
tta tct tct gat gca cca ggg gtg cca agg att gaa gaa gaa aag tcg Leu Ser Ser Asp Ala Pro Gly Val Pro Arg Ile Glu Glu Glu Lys Ser 145 150 155	483
gaa gag gag act tca gcc cct gcc atc acc act gtg aca gtg cca act Glu Glu Glu Thr Ser Ala Pro Ala Ile Thr Thr Val Thr Val Pro Thr 160 165 170	531
ccg att tac cag aca agc agt ggg cag tat att gcc att acc cag gga Pro Ile Tyr Gln Thr Ser Ser Gly Gln Tyr Ile Ala Ile Thr Gln Gly 175 180 185	579
gga gct ata cag ctg gct aac aat ggt acc gat ggg gta cag ggc ctt Gly Ala Ile Gln Leu Ala Asn Asn Gly Thr Asp Gly Val Gln Gly Leu 190 195 200	627
cag aca tta acc atg acc aat gca gct gcc act cag ccg ggt acc act Gln Thr Leu Thr Met Thr Asn Ala Ala Thr Gln Pro Gly Thr Thr 205 210 215 220	675
att cta cag tat gca cag acc act gat gga cag cag att cta gtg ccc Ile Leu Gln Tyr Ala Gln Thr Thr Asp Gly Gln Gln Ile Leu Val Pro 225 230 235	723
agc aac caa gtt gtt gtt caa gct tct ggc gat gta caa aca tac Ser Asn Gln Val Val Gln Ala Ala Ser Gly Asp Val Gln Thr Tyr 240 245 250	771
caa att cgt aca gca ccc act agc acc atc gcc cct gga gtt gtt atg Gln Ile Arg Thr Ala Pro Thr Ser Thr Ile Ala Pro Gly Val Val Met 255 260 265	819
gca tcc tcc cca gca ctt cct acg cag cct gct gaa gaa gca gcc cg Ala Ser Ser Pro Ala Leu Pro Thr Gln Pro Ala Glu Glu Ala Ala Arg 270 275 280	867
aag aga gag gtt cgt cta atg aag aac agg gaa gca gca aga gaa tgt Lys Arg Glu Val Arg Leu Met Lys Asn Arg Glu Ala Ala Arg Glu Cys 285 290 295 300	915
cgt aga aag aag aaa gaa tat gtg aaa tgt tta gag aac aga gtg gca Arg Arg Lys Lys Lys Glu Tyr Val Lys Cys Leu Glu Asn Arg Val Ala 305 310 315	963

SequenceListing-73670826.txt

gtg ctt gaa aac caa aac aag aca ttg att gag gag cta aaa gca ctt	1011
Val Leu Glu Asn Gln Asn Lys Thr Leu Ile Glu Glu Leu Lys Ala Leu	
320 325 330	

aag gac ctt tac tgc cac aaa tca gat taaggatcc	1047
Lys Asp Leu Tyr Cys His Lys Ser Asp	
335 340	

<210> 43  
<211> 1047  
<212> DNA  
<213> Cricetulus longicaudatus

<220>  
<221> CDS  
<222> (16)..(1038)

aagcttgcgg ccacc atg acc atg gaa tct gga gca gac aac cag cag agt	51
Met Thr Met Glu Ser Gly Ala Asp Asn Gln Gln Ser	
1 5 10	

gga gat gct gct gta aca gaa gct gaa aat caa caa atg aca gct caa	99
Gly Asp Ala Ala Val Thr Glu Ala Glu Asn Gln Gln Met Thr Ala Gln	
15 20 25	

gcc caa cca cag att gcc aca tta gcc cag gta tcc atg cca gca gct	147
Ala Gln Pro Gln Ile Ala Thr Leu Ala Gln Val Ser Met Pro Ala Ala	
30 35 40	

cat gcg aca tca tct gct ccc act gta acc tta gtg cag ctg ccc aat	195
His Ala Thr Ser Ser Ala Pro Thr Val Thr Leu Val Gln Leu Pro Asn	
45 50 55 60	

ggg cag aca gtc caa gtc cat gga gtt att cag gcg gcc cag cca tca	243
Gly Gln Thr Val Gln Val His Gly Val Ile Gln Ala Ala Gln Pro Ser	
65 70 75	

gtt att cag tct cca caa gtc caa aca gtt cag tct tcc tgt aag gac	291
Val Ile Gln Ser Pro Gln Val Gln Thr Val Gln Ser Ser Cys Lys Asp	
80 85 90	

tta aaa aga ctt ttc tcc gga act cag att tca act att gca gaa agt	339
Leu Lys Arg Leu Phe Ser Gly Thr Gln Ile Ser Thr Ile Ala Glu Ser	
95 100 105	

gag gat tca cag gaa tct gtg gat agt gta act gat tcc caa aag cga	387
Glu Asp Ser Gln Glu Ser Val Asp Ser Val Thr Asp Ser Gln Lys Arg	
110 115 120	

agg gaa att ctt tca agg agg cct tcc tcc agg aaa att ttg aat gac	435
Arg Glu Ile Leu Ser Arg Arg Pro Ser Ser Arg Lys Ile Leu Asn Asp	
125 130 135 140	

tta tct tct gat gca cca ggg gtg cca agg att gaa gaa gaa aag tcg	483
Leu Ser Ser Asp Ala Pro Gly Val Pro Arg Ile Glu Glu Glu Lys Ser	
145 150 155	

gaa gag gag act tca gcc cct gcc atc acc act gtg aca gtg cca act	531
Glu Glu Glu Thr Ser Ala Pro Ala Ile Thr Thr Val Thr Val Pro Thr	

## SequenceListing-73670826.txt

160

165

170

579

ccg att tac cag aca agc agt ggg cag tat att gcc att acc cag gga  
 Pro Ile Tyr Gln Thr Ser Ser Gly Gln Tyr Ile Ala Ile Thr Gln Gly  
 175 180 185

627

gga gct ata cag ctg gct aac aat ggt acc gat ggg gta cag ggc ctt  
 Gly Ala Ile Gln Leu Ala Asn Asn Gly Thr Asp Gly Val Gln Gly Leu  
 190 195 200

675

cag aca tta acc atg acc aat gca gct gcc act cag ccg ggt acc act  
 Gln Thr Leu Thr Met Thr Asn Ala Ala Ala Thr Gln Pro Gly Thr Thr  
 205 210 215 220

att cta cag tat gca cag acc act gat gga cag cag att cta gtg ccc  
 Ile Leu Gln Tyr Ala Gln Thr Thr Asp Gly Gln Gln Ile Leu Val Pro  
 225 230 235

723

agc aaccaa gtt gtt caa gct gcc tct ggc gat gta caa aca tac  
 Ser Asn Gln Val Val Gln Ala Ala Ser Gly Asp Val Gln Thr Tyr  
 240 245 250

771

caa att cgt aca gca ccc act agc acc atc gcc cct gga gtt gtt atg  
 Gln Ile Arg Thr Ala Pro Thr Ser Thr Ile Ala Pro Gly Val Val Met  
 255 260 265

819

gca tcc tcc cca gca ctt cct acg cag cct gct gaa gaa gca gcc cgg  
 Ala Ser Ser Pro Ala Leu Pro Thr Gln Pro Ala Glu Glu Ala Ala Arg  
 270 275 280

867

aag aga gag gtt cgt cta atg aag aac agg gaa gca gca aga gaa tgt  
 Lys Arg Glu Val Arg Leu Met Lys Asn Arg Glu Ala Ala Arg Glu Cys  
 285 290 295 300

915

cgt aga aag aag aaa gaa tat gtg aaa tgt tta gag aac aga gtg gca  
 Arg Arg Lys Lys Lys Glu Tyr Val Lys Cys Leu Glu Asn Arg Val Ala  
 305 310 315

963

gtg ctt gaa aac caa aac aag aca ttg att gag gag cta aaa gca ctt  
 Val Leu Glu Asn Gln Asn Lys Thr Leu Ile Glu Glu Leu Lys Ala Leu  
 320 325 330

1011

aag gac ctt tac tgc cac aaa tca gat taaggatcc  
 Lys Asp Leu Tyr Cys His Lys Ser Asp  
 335 340

1047

<210> 44  
<211> 564  
<212> DNA  
<213> Human adenovirus type 5

<220>  
<221> CDS  
<222> (28)..(555)

<400> 44  
aagcttactg ttggtaaagc cgccacc atg gag gct tgg gag tgt ttg gaa gat  
Met Glu Ala Trp Glu Cys Leu Glu Asp  
1 5

54

ttt tct gct gtg cgt aac ttg ctg gaa cag agc tct aac agt acc tct  
102

SequenceListing-73670826.txt

Phe Ser Ala Val Arg Asn Leu Leu Glu Gln Ser Ser Asn Ser Thr Ser 10	15	20	25		
tgg ttt tgg agg ttt ctg tgg ggc tca tcc cag gca aag tta gtc tgc Trp Phe Trp Arg Phe Leu Trp Gly Ser Ser Gln Ala Lys Leu Val Cys 30	35		40	150	
aga att aag gag gat tac aag tgg gaa ttt gaa gag ctt ttg aaa tcc Arg Ile Lys Glu Asp Tyr Lys Trp Glu Phe Glu Glu Leu Leu Lys Ser 45	50		55	198	
tgt ggt gag ctg ttt gat tct ttg aat ctg ggt cac cag gcg ctt ttc Cys Gly Glu Leu Phe Asp Ser Leu Asn Leu Gly His Gln Ala Leu Phe 60	65		70	246	
caa gag aag gtc atc aag act ttg gat ttt tcc aca ccg ggg cgcc gct Gln Glu Lys Val Ile Lys Thr Leu Asp Phe Ser Thr Pro Gly Arg Ala 75	80		85	294	
gcg gct gct gtt gct ttt ttg agt ttt ata aag gat aaa tgg agc gaa Ala Ala Ala Val Ala Phe Leu Ser Phe Ile Lys Asp Lys Trp Ser Glu 90	95		100	105	342
gaa acc cat ctg agc ggg ggg tac ctg ctg gat ttt ctg gcc atg cat Glu Thr His Leu Ser Gly Gly Tyr Leu Leu Asp Phe Leu Ala Met His 110	115		120		390
ctg tgg aga gcg gtt gtg aga cac aag aat cgc ctg cta ctg ttg tct Leu Trp Arg Ala Val Val Arg His Lys Asn Arg Leu Leu Leu Leu Ser 125	130		135		438
tcc gtc cgc ccg gcg ata ata ccg acg gag gag cag cag cag cag cag Ser Val Arg Pro Ala Ile Ile Pro Thr Glu Glu Gln Gln Gln Gln Gln 140	145		150		486
gag gaa gcc agg cgg cgg cag gag cag agc cca tgg aac ccg aga Glu Glu Ala Arg Arg Arg Gln Glu Gln Ser Pro Trp Asn Pro Arg 155	160		165		534
gcc ggc ctg gac cct cgg gaa tgatctaga Ala Gly Leu Asp Pro Arg Glu 170	175				564

<210> 45  
<211> 596  
<212> DNA  
<213> Cricetulus longicaudatus

<220>				
<221> CDS				
<222> (3)..(587)				
<400> 45				
cc atg gct caa gct ggg aga aca ggg tat gat aac cga gag atc gtg Met Ala Gln Ala Gly Arg Thr Gly Tyr Asp Asn Arg Glu Ile Val 1	5	10	15	47
atg aag tac atc cat tat aag ctg tca cag agg ggc tac gag tgg gat Met Lys Tyr Ile His Tyr Lys Leu Ser Gln Arg Gly Tyr Glu Trp Asp 20	25		30	95

SequenceListing-73670826.txt

gtg gga gat gtg gac gcc gcg gcc gcg gcc agc ccc gtg cca cct Val Gly Asp Val Asp Ala Ala Ala Ala Ala Ser Pro Val Pro Pro	143
35 40 45	
gtg gtc cac ctg acc ctc cgc cg <sup>g</sup> gct ggg gat gac ttc tcc cgt cgc Val Val His Leu Thr Leu Arg Arg Ala Gly Asp Asp Phe Ser Arg Arg	191
50 55 60	
tac cgt cgc gac ttc gc <sup>g</sup> gag atg tcc agt cag ctg cac ctg acg ccc Tyr Arg Arg Asp Phe Ala Glu Met Ser Ser Gln Leu His Leu Thr Pro	239
65 70 75	
ttc acc gc <sup>g</sup> agg gga cgc ttt gct acg gtg gtg gag gaa ctc ttc agg Phe Thr Ala Arg Gly Arg Phe Ala Thr Val Val Glu Glu Leu Phe Arg	287
80 85 90 95	
gat ggg gtg aac tgg ggg agg att gtg gcc ttc ttt gag ttc ggt ggg Asp Gly Val Asn Trp Gly Arg Ile Val Ala Phe Phe Glu Phe Gly Gly	335
100 105 110	
gtc atg tgt gtg gag agc gtc aac agg gag atg tca ccc ctg gtg gac Val Met Cys Val Glu Ser Val Asn Arg Glu Met Ser Pro Leu Val Asp	383
115 120 125	
aac atc gcc ctg tgg atg acc gag tac ctg aac cgg cat ctg cac acc Asn Ile Ala Leu Trp Met Thr Glu Tyr Leu Asn Arg His Leu His Thr	431
130 135 140	
tgg atc cag gat aac gga ggc tgg gac gca ttt gtg gaa ctg tac ggc Trp Ile Gln Asp Asn Gly Gly Trp Asp Ala Phe Val Glu Leu Tyr Gly	479
145 150 155	
ccc agt gtg agg cct ctg ttt gat ttc tct tgg ctg tct ctg aag acc Pro Ser Val Arg Pro Leu Phe Asp Phe Ser Trp Leu Ser Leu Lys Thr	527
160 165 170 175	
ctg ctc agc ctg gcc ctg gtc ggg gcc tgc atc act ctg ggt acc tac Leu Leu Ser Leu Ala Leu Val Gly Ala Cys Ile Thr Leu Gly Thr Tyr	575
180 185 190	
ctg ggc cac aag tgatctaga Leu Gly His Lys	596
195	

<210> 46  
<211> 37  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic primer

<400> 46  
cg<sup>c</sup>acta gtttatggcc tggggcg<sup>t</sup>ttt acagctc 37

<210> 47  
<211> 20  
<212> DNA  
<213> Artificial Sequence

SequenceListing-73670826.txt

<220>  
<223> Description of Artificial sequence: Synthetic  
primer

<400> 47  
gagctattcc agaagtatgtg

20

<210> 48  
<211> 289  
<212> PRT  
<213> Human adenovirus type 5

<400> 48  
Met Arg His Ile Ile Cys His Gly Gly Val Ile Thr Glu Glu Met Ala  
1 5 10 15

Ala Ser Leu Leu Asp Gln Leu Ile Glu Glu Val Leu Ala Asp Asn Leu  
20 25 30

Pro Pro Pro Ser His Phe Glu Pro Pro Thr Leu His Glu Leu Tyr Asp  
35 40 45

Leu Asp Val Thr Ala Pro Glu Asp Pro Asn Glu Glu Ala Val Ser Gln  
50 55 60

Ile Phe Pro Asp Ser Val Met Leu Ala Val Gln Glu Gly Ile Asp Leu  
65 70 75 80

Leu Thr Phe Pro Pro Ala Pro Gly Ser Pro Glu Pro Pro His Leu Ser  
85 90 95

Arg Gln Pro Glu Gln Pro Glu Gln Arg Ala Leu Gly Pro Val Ser Met  
100 105 110

Pro Asn Leu Val Pro Glu Val Ile Asp Leu Thr Cys His Glu Ala Gly  
115 120 125

Phe Pro Pro Ser Asp Asp Glu Asp Glu Glu Gly Glu Glu Phe Val Leu  
130 135 140

Asp Tyr Val Glu His Pro Gly His Gly Cys Arg Ser Cys His Tyr His  
145 150 155 160

Arg Arg Asn Thr Gly Asp Pro Asp Ile Met Cys Ser Leu Cys Tyr Met  
165 170 175

Arg Thr Cys Gly Met Phe Val Tyr Ser Pro Val Ser Glu Pro Glu Pro  
180 185 190

SequenceListing-73670826.txt  
Glu Pro Glu Pro Glu Pro Glu Pro Ala Arg Pro Thr Arg Arg Pro Lys  
195 200 205

Met Ala Pro Ala Ile Leu Arg Arg Pro Thr Ser Pro Val Ser Arg Glu  
210 215 220

Cys Asn Ser Ser Thr Asp Ser Cys Asp Ser Gly Pro Ser Asn Thr Pro  
225 230 235 240

Pro Glu Ile His Pro Val Val Pro Leu Cys Pro Ile Lys Pro Val Ala  
245 250 255

Val Arg Val Gly Gly Arg Arg Gln Ala Val Glu Cys Ile Glu Asp Leu  
260 265 270

Leu Asn Glu Pro Gly Gln Pro Leu Asp Leu Ser Cys Lys Arg Pro Arg  
275 280 285

Pro

<210> 49  
<211> 289  
<212> PRT  
<213> Human adenovirus type 5

<400> 49  
Met Arg His Ile Ile Cys His Gly Gly Val Ile Thr Glu Glu Met Ala  
1 5 10 15

Ala Ser Leu Leu Asp Gln Leu Ile Glu Glu Val Leu Ala Asp Asn Leu  
20 25 30

Pro Pro Pro Ser His Phe Glu Pro Pro Thr Leu His Glu Leu His Asp  
35 40 45

Leu Asp Val Thr Ala Pro Glu Asp Pro Asn Glu Glu Ala Val Ser Gln  
50 55 60

Ile Phe Pro Asp Ser Val Met Leu Ala Val Gln Glu Gly Ile Asp Leu  
65 70 75 80

Leu Thr Phe Pro Pro Ala Pro Gly Ser Pro Glu Pro Pro His Leu Ser  
85 90 95

Arg Gln Pro Glu Gln Pro Glu Gln Arg Ala Leu Gly Pro Val Ser Met  
100 105 110

Pro Asn Leu Val Pro Glu Val Ile Asp Leu Thr Cys His Glu Ala Gly

115

SequenceListing-73670826.txt  
120 125

Phe Pro Pro Ser Asp Asp Glu Asp Glu Glu Gly Glu Glu Phe Val Leu  
130 135 140

Asp Tyr Val Glu His Pro Gly His Gly Cys Arg Ser Cys His Tyr His  
145 150 155 160

Arg Arg Asn Thr Gly Asp Pro Asp Ile Met Cys Ser Leu Cys Tyr Met  
165 170 175

Arg Thr Cys Gly Met Phe Val Tyr Ser Pro Val Ser Glu Pro Glu Pro  
180 185 190

Glu Pro Glu Pro Glu Pro Ala Arg Pro Thr Arg Arg Pro Lys  
195 200 205

Met Ala Pro Ala Ile Leu Arg Arg Pro Thr Ser Pro Val Ser Arg Glu  
210 215 220

Cys Asn Ser Ser Thr Asp Ser Cys Asp Ser Gly Pro Ser Asn Thr Pro  
225 230 235 240

Pro Glu Ile His Pro Val Val Pro Leu Cys Pro Ile Lys Pro Val Ala  
245 250 255

Val Arg Val Gly Gly Arg Arg Gln Ala Val Glu Cys Ile Glu Asp Leu  
260 265 270

Leu Asn Glu Pro Gly Gln Pro Leu Asp Leu Ser Cys Lys Arg Pro Arg  
275 280 285

Pro

<210> 50  
<211> 341  
<212> PRT  
<213> Cricetulus longicaudatus

<400> 50  
Met Thr Met Glu Ser Gly Ala Asp Asn Gln Gln Ser Gly Asp Ala Ala  
1 5 10 15

Val Thr Glu Ala Glu Asn Gln Gln Met Thr Ala Gln Ala Gln Pro Gln  
20 25 30

Ile Ala Thr Leu Ala Gln Val Ser Met Pro Ala Ala His Ala Thr Ser  
35 40 45

SequenceListing-73670826.txt

Ser Ala Pro Thr Val Thr Leu Val Gln Leu Pro Asn Gly Gln Thr Val  
50 55 60

Gln Val His Gly Val Ile Gln Ala Ala Gln Pro Ser Val Ile Gln Ser  
65 70 75 80

Pro Gln Val Gln Thr Val Gln Ser Ser Cys Lys Asp Leu Lys Arg Leu  
85 90 95

Phe Ser Gly Thr Gln Ile Ser Thr Ile Ala Glu Ser Glu Asp Ser Gln  
100 105 110

Glu Ser Val Asp Ser Val Thr Asp Ser Gln Lys Arg Arg Glu Ile Leu  
115 120 125

Ser Arg Arg Pro Ser Tyr Arg Lys Ile Leu Asn Asp Leu Ser Ser Asp  
130 135 140

Ala Pro Gly Val Pro Arg Ile Glu Glu Glu Lys Ser Glu Glu Glu Thr  
145 150 155 160

Ser Ala Pro Ala Ile Thr Thr Val Thr Val Pro Thr Pro Ile Tyr Gln  
165 170 175

Thr Ser Ser Gly Gln Tyr Ile Ala Ile Thr Gln Gly Gly Ala Ile Gln  
180 185 190

Leu Ala Asn Asn Gly Thr Asp Gly Val Gln Gly Leu Gln Thr Leu Thr  
195 200 205

Met Thr Asn Ala Ala Ala Thr Gln Pro Gly Thr Thr Ile Leu Gln Tyr  
210 215 220

Ala Gln Thr Thr Asp Gly Gln Gln Ile Leu Val Pro Ser Asn Gln Val  
225 230 235 240

Val Val Gln Ala Ala Ser Gly Asp Val Gln Thr Tyr Gln Ile Arg Thr  
245 250 255

Ala Pro Thr Ser Thr Ile Ala Pro Gly Val Val Met Ala Ser Ser Pro  
260 265 270

Ala Leu Pro Thr Gln Pro Ala Glu Glu Ala Ala Arg Lys Arg Glu Val  
275 280 285

Arg Leu Met Lys Asn Arg Glu Ala Ala Arg Glu Cys Arg Arg Lys Lys

## SequenceListing-73670826.txt

290

295

300

Lys Glu Tyr Val Lys Cys Leu Glu Asn Arg Val Ala Val Leu Glu Asn  
 305                   310                   315                   320

Gln Asn Lys Thr Leu Ile Glu Glu Leu Lys Ala Leu Lys Asp Leu Tyr  
 325                   330                   335

Cys His Lys Ser Asp  
 340

<210> 51  
<211> 341  
<212> PRT  
<213> Cricetulus longicaudatus

<400> 51  
Met Thr Met Glu Ser Gly Ala Asp Asn Gln Gln Ser Gly Asp Ala Ala  
 1               5                   10               15

Val Thr Glu Ala Glu Asn Gln Gln Met Thr Ala Gln Ala Gln Pro Gln  
 20               25                   30

Ile Ala Thr Leu Ala Gln Val Ser Met Pro Ala Ala His Ala Thr Ser  
 35               40                   45

Ser Ala Pro Thr Val Thr Leu Val Gln Leu Pro Asn Gly Gln Thr Val  
 50               55                   60

Gln Val His Gly Val Ile Gln Ala Ala Gln Pro Ser Val Ile Gln Ser  
 65               70                   75               80

Pro Gln Val Gln Thr Val Gln Ser Ser Cys Lys Asp Leu Lys Arg Leu  
 85               90                   95

Phe Ser Gly Thr Gln Ile Ser Thr Ile Ala Glu Ser Gly Asp Ser Gln  
 100              105                   110

Glu Ser Val Asp Ser Val Thr Asp Ser Gln Lys Arg Arg Glu Ile Leu  
 115              120                   125

Ser Arg Arg Pro Ser Ser Arg Lys Ile Leu Asn Asp Leu Ser Ser Asp  
 130              135                   140

Ala Pro Gly Val Pro Arg Ile Glu Glu Glu Lys Ser Glu Glu Glu Thr  
 145              150                   155               160

Ser Ala Pro Ala Ile Thr Thr Val Thr Val Pro Thr Pro Ile Tyr Gln  
 165              170                   175

SequenceListing-73670826.txt

Thr Ser Ser Gly Gln Tyr Ile Ala Ile Thr Gln Gly Gly Ala Ile Gln  
180 185 190

Leu Ala Asn Asn Gly Thr Asp Gly Val Gln Gly Leu Gln Thr Leu Thr  
195 200 205

Met Thr Asn Ala Ala Ala Thr Gln Pro Gly Thr Thr Ile Leu Gln Tyr  
210 215 220

Ala Gln Thr Thr Asp Gly Gln Gln Ile Leu Val Pro Ser Asn Gln Val  
225 230 235 240

Val Val Gln Ala Ala Ser Gly Asp Val Gln Thr Tyr Gln Ile Arg Thr  
245 250 255

Ala Pro Thr Ser Thr Ile Ala Pro Gly Val Val Met Ala Ser Ser Pro  
260 265 270

Ala Leu Pro Thr Gln Pro Ala Glu Glu Ala Ala Arg Lys Arg Glu Val  
275 280 285

Arg Leu Met Lys Asn Arg Glu Ala Ala Arg Glu Cys Arg Arg Lys Lys  
290 295 300

Lys Glu Tyr Val Lys Cys Leu Glu Asn Arg Val Ala Val Leu Glu Asn  
305 310 315 320

Gln Asn Lys Thr Leu Ile Glu Glu Leu Lys Ala Leu Lys Asp Leu Tyr  
325 330 335

Cys His Lys Ser Asp  
340

<210> 52

<211> 176

<212> PRT

<213> Human adenovirus type 5

<400> 52

Met Glu Ala Trp Glu Cys Leu Glu Asp Phe Ser Ala Val Arg Asn Leu  
1 5 10 15

Leu Glu Gln Ser Ser Asn Ser Thr Ser Trp Phe Trp Arg Phe Leu Trp  
20 25 30

Gly Ser Ser Gln Ala Lys Leu Val Cys Arg Ile Lys Glu Asp Tyr Lys  
35 40 45

SequenceListing-73670826.txt

Trp Glu Phe Glu Glu Leu Leu Lys Ser Cys Gly Glu Leu Phe Asp Ser  
50 55 60

Leu Asn Leu Gly His Gln Ala Leu Phe Gln Glu Lys Val Ile Lys Thr  
65 70 75 80

Leu Asp Phe Ser Thr Pro Gly Arg Ala Ala Ala Ala Val Ala Phe Leu  
85 90 95

Ser Phe Ile Lys Asp Lys Trp Ser Glu Glu Thr His Leu Ser Gly Gly  
100 105 110

Tyr Leu Leu Asp Phe Leu Ala Met His Leu Trp Arg Ala Val Val Arg  
115 120 125

His Lys Asn Arg Leu Leu Leu Ser Ser Val Arg Pro Ala Ile Ile  
130 135 140

Pro Thr Glu Glu Gln Gln Gln Gln Glu Glu Ala Arg Arg Arg Arg  
145 150 155 160

Gln Glu Gln Ser Pro Trp Asn Pro Arg Ala Gly Leu Asp Pro Arg Glu  
165 170 175

<210> 53

<211> 195

<212> PRT

<213> Cricetulus longicaudatus

<400> 53

Met Ala Gln Ala Gly Arg Thr Gly Tyr Asp Asn Arg Glu Ile Val Met  
1 5 10 15

Lys Tyr Ile His Tyr Lys Leu Ser Gln Arg Gly Tyr Glu Trp Asp Val  
20 25 30

Gly Asp Val Asp Ala Ala Ala Ala Ala Ser Pro Val Pro Pro Val  
35 40 45

Val His Leu Thr Leu Arg Arg Ala Gly Asp Asp Phe Ser Arg Arg Tyr  
50 55 60

Arg Arg Asp Phe Ala Glu Met Ser Ser Gln Leu His Leu Thr Pro Phe  
65 70 75 80

Thr Ala Arg Gly Arg Phe Ala Thr Val Val Glu Glu Leu Phe Arg Asp  
85 90 95

SequenceListing-73670826.txt  
Gly Val Asn Trp Gly Arg Ile Val Ala Phe Phe Glu Phe Gly Gly Val  
100 105 110

Met Cys Val Glu Ser Val Asn Arg Glu Met Ser Pro Leu Val Asp Asn  
115 120 125

Ile Ala Leu Trp Met Thr Glu Tyr Leu Asn Arg His Leu His Thr Trp  
130 135 140

Ile Gln Asp Asn Gly Gly Trp Asp Ala Phe Val Glu Leu Tyr Gly Pro  
145 150 155 160

Ser Val Arg Pro Leu Phe Asp Phe Ser Trp Leu Ser Leu Lys Thr Leu  
165 170 175

Leu Ser Leu Ala Leu Val Gly Ala Cys Ile Thr Leu Gly Thr Tyr Leu  
180 185 190

Gly His Lys  
195

<210> 54  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic peptide

<400> 54  
Arg Ser Val Leu Thr Arg  
1 5

<210> 55  
<211> 5  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic peptide

<400> 55  
Gly Gly Gly Gly Ser  
1 5

<210> 56  
<211> 12  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic

SequenceListing-73670826.txt

peptide

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